

SEQUENCE LISTING

<110> SCHWAEBLE, Wilhelm
University of Leicester, The

<120> Clq and Collectin Receptor

<130> M97/0287/PCT

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<170> PatentIn Ver. 2.0

<210> 1

<211> 122

<212> PRT

<213> Homo sapiens

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Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val Arg
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20 25 30

Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile Lys
35 40 45

Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys Ile
50 55 60

Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu His
65 70 75 80

Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu Met
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Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys Gly
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Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro
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Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro
115 120

<210> 3.

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<212> PRT

<213> Rattus norvegicus

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Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu Met
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Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys Gly
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Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro
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<210> 4

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<212> DNA

<213> Homo sapiens

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ttcctgccac ccaagaagat aaaggatcct gatgcttcaa aaccggaaga ctgggatgag 180

cgggccaaga tcgatgatcc cacagactcc aagcctgagg actgggacaa gcccgagcat 240

atccctgacc ctgatgctaa gaagcccgag gactgggatg aagagatgga cggagagtgg 300

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366

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tttctgccac ccaagaagat aaaggaccct gatgctgcca agccggaaga ctgggatgaa 180

cgagccaaga tcgatgaccc cacagattcc aagcctgagg actgggacaa gccagagcac 240

atccctgacc ctgatgctaa gaagcctgag gactgggatg aagagatgga tggagagtgg 300

gaaccaccag tgattcaaaa tcttgaatac aagggtgagt ggaaaccacg tcaattgac 360

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<213> Rattus norvegicus

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tttctgccgc ccaagaagat taaggatcct gacgctgcca agccagaaga ctgggatgaa 180

cgagccaaga ttgatgaccc cacagattcc aagcctgagg actgggacaa gccagagcac 240

atccctgacc ctgatgctaa gaagcctgag gactgggacg aagagatgga tggagagtgg 300

gaaccaccag tgattcaaaa tcttgaatac aagggcgaat ggaagccacg tcaaattgac 360

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366

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<212> PRT

<213> Homo sapiens

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			20					25					30		

Trp	Thr	Pro	Arg	Trp	Ile	Glu	Ser	Lys	His	Lys	Ser	Asp	Phe	Gly	Lys
		35						40				45			

Phe	Val	Leu	Ser	Ser	Gly	Lys	Phe	Tyr	Gly	Asp	Glu	Glu	Lys	Asp	Lys
	50					55					60				

Gly	Leu	Gln	Thr	Ser	Gln	Asp	Ala	Arg	Phe	Tyr	Ala	Leu	Ser	Ala	Ser
65					70					75				80	

Phe	Glu	Pro	Phe	Ser	Asn	Lys	Gly	Gln	Thr	Leu	Val	Val	Gln	Phe	Thr
				85					90					95	

Val	Lys	His	Glu	Gln	Asn	Ile	Asp	Cys	Gly	Gly	Gly	Tyr	Val	Lys	Leu
		100						105					110		

Phe	Pro	Asn	Ser	Leu	Asp	Gln	Thr	Asp	Met	His	Gly	Asp	Ser	Glu	Tyr
		115					120					125			

Asn	Ile	Met	Phe	Gly	Pro	Asp	Ile	Cys	Gly	Pro	Gly	Thr	Lys	Lys	Val
	130					135					140				

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp
145 150 155 160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
165 170 175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
180 185 190

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
195 200 205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
210 215 220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu
225 230 235 240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu
245 250 255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys
260 265 270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Pro Ser
290 295 300

Ile Tyr Ala Tyr Asp Asn Phe Gly Val Leu Gly Leu Asp Leu Trp Gln
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Ala
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys
355 360 365

Glu Glu Glu Glu Asp Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Asp
370 375 380

Lys Glu Asp Asp Glu Asp Lys Asp Glu Asp Glu Glu Asp Glu Glu Asp
385 390 395 400

Lys Glu Glu Asp Glu Glu Glu Asp Val Pro Gly Gln Ala Lys Asp Glu
405 410 415

Leu